

Journal club: April 09, 2013

Genome Engineering Using CRISPR

RNA-Guided Human Genome Engineering via Cas9

Prashant Mali,^{1*} Luhan Yang,^{1,3*} Kevin M. Esvelt,² John Aach,¹ Marc Guell,¹ James E. DiCarlo,⁴ Julie E. Norville,¹ George M. Church^{1,2†}

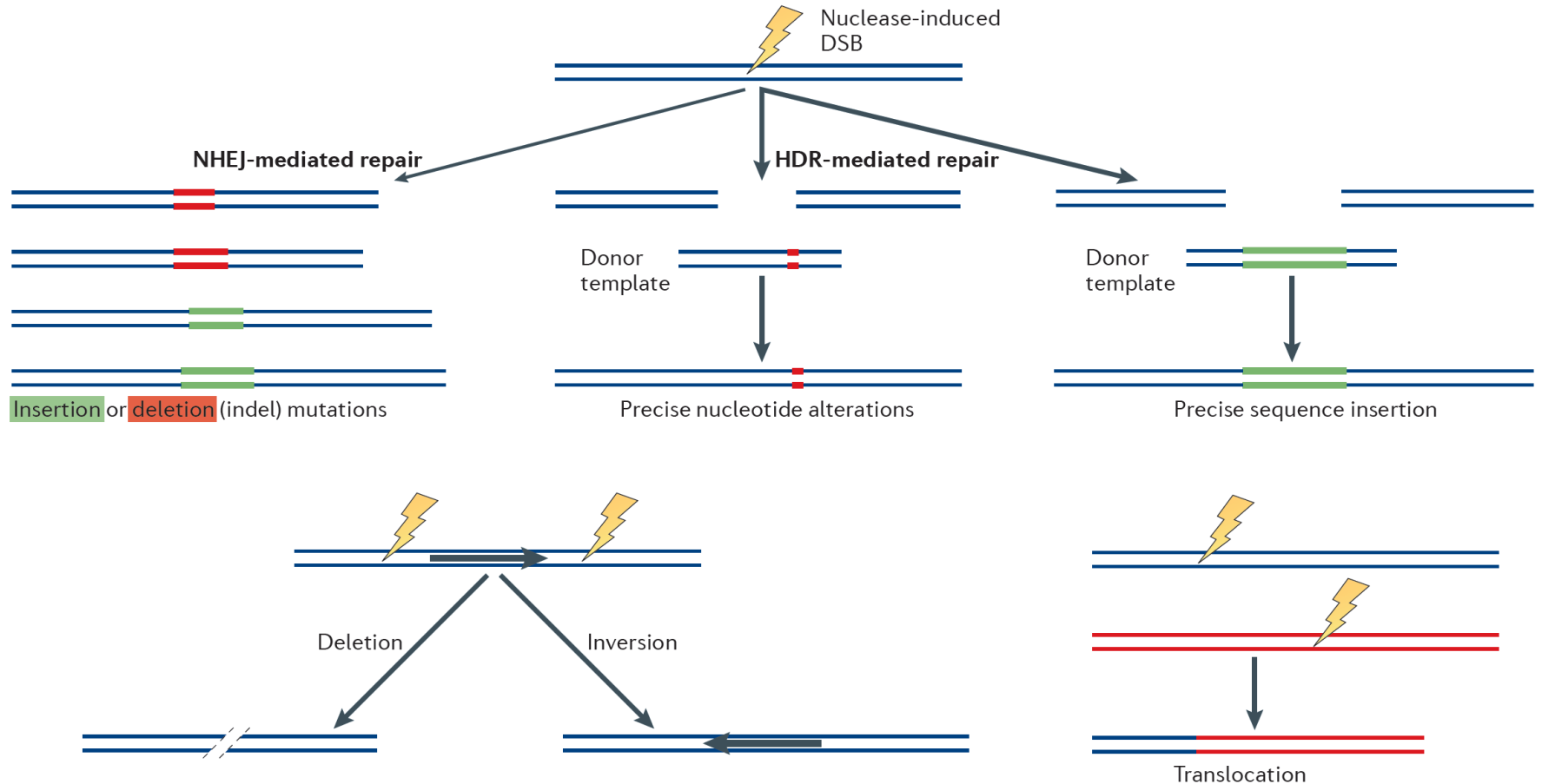
SCIENCE VOL 339 15 FEBRUARY 2013

Multiplex Genome Engineering Using CRISPR/Cas Systems

Le Cong,^{1,2*} F. Ann Ran,^{1,4*} David Cox,^{1,3} Shuailiang Lin,^{1,5} Robert Barretto,⁶ Naomi Habib,¹ Patrick D. Hsu,^{1,4} Xuebing Wu,⁷ Wenyan Jiang,⁸ Luciano A. Marraffini,⁸ Feng Zhang^{1†}

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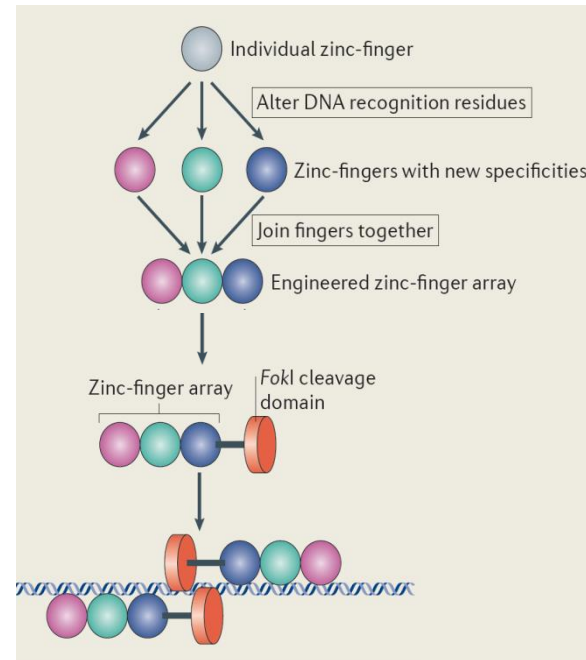
background - genome editing



genome editing – how to induce DSB?

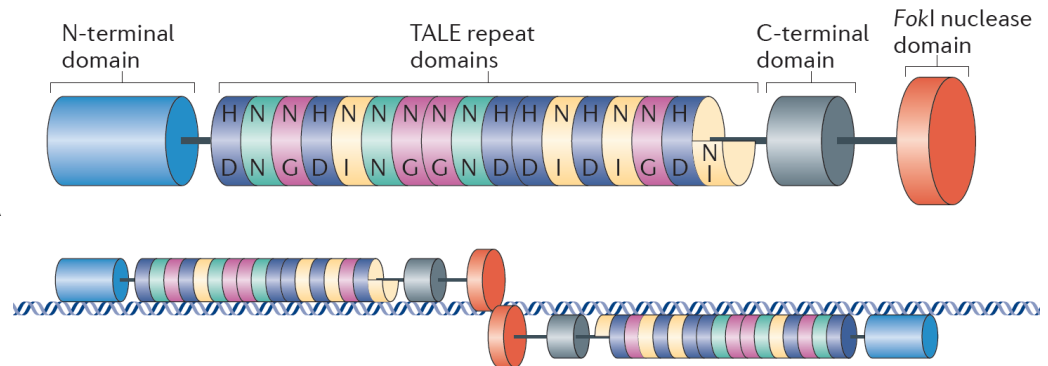
zinc-finger nucleases (ZFNs)

- Cys2His2 DNA binding-domains
- recognize approx. 3 bp
- modifying DNA binding specificity
- array-design
- fusion with nonspecific endonuclease domain



transcription activator-like effector nucleases (TALENs)

- 33-35 aa bacterial repeats
- specifically binding to 1 base of DNA
- array-design
- fusion with nonspecific endonuclease domain



J. Keith Joungh and Jeffry D. Sander

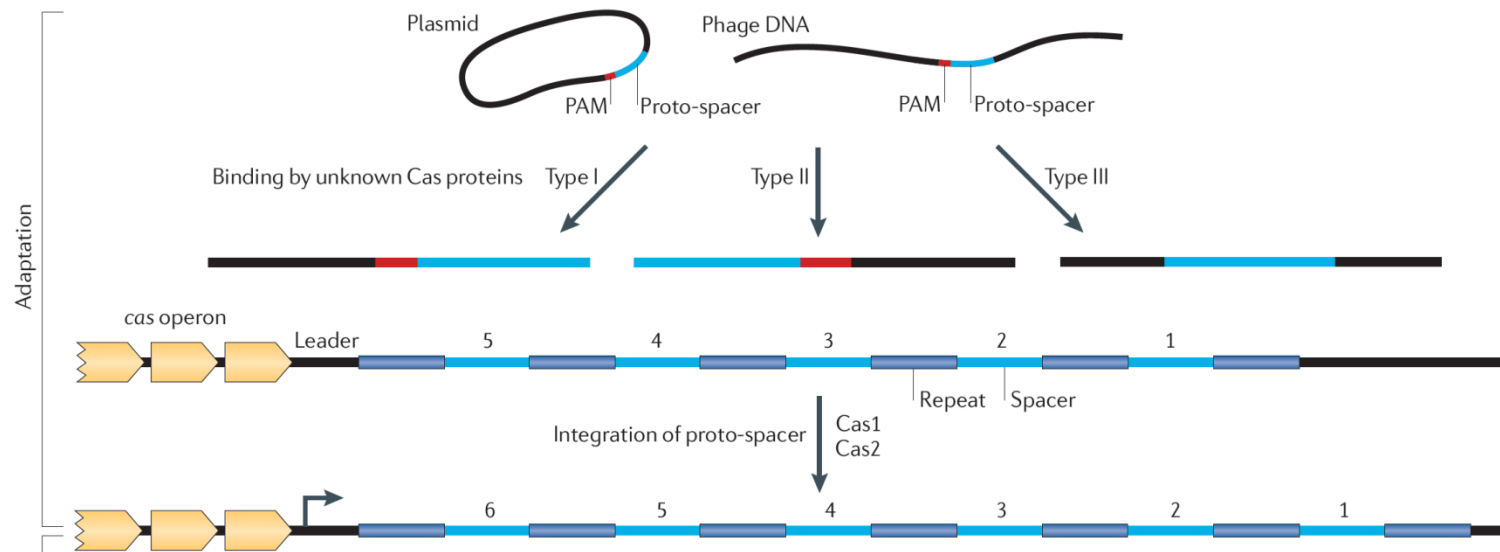
NATURE REVIEWS | MOLECULAR CELL BIOLOGY

VOLUME 14 | JANUARY 2013

background - CRISPR

the adaptive immune system of bacteria and archaea

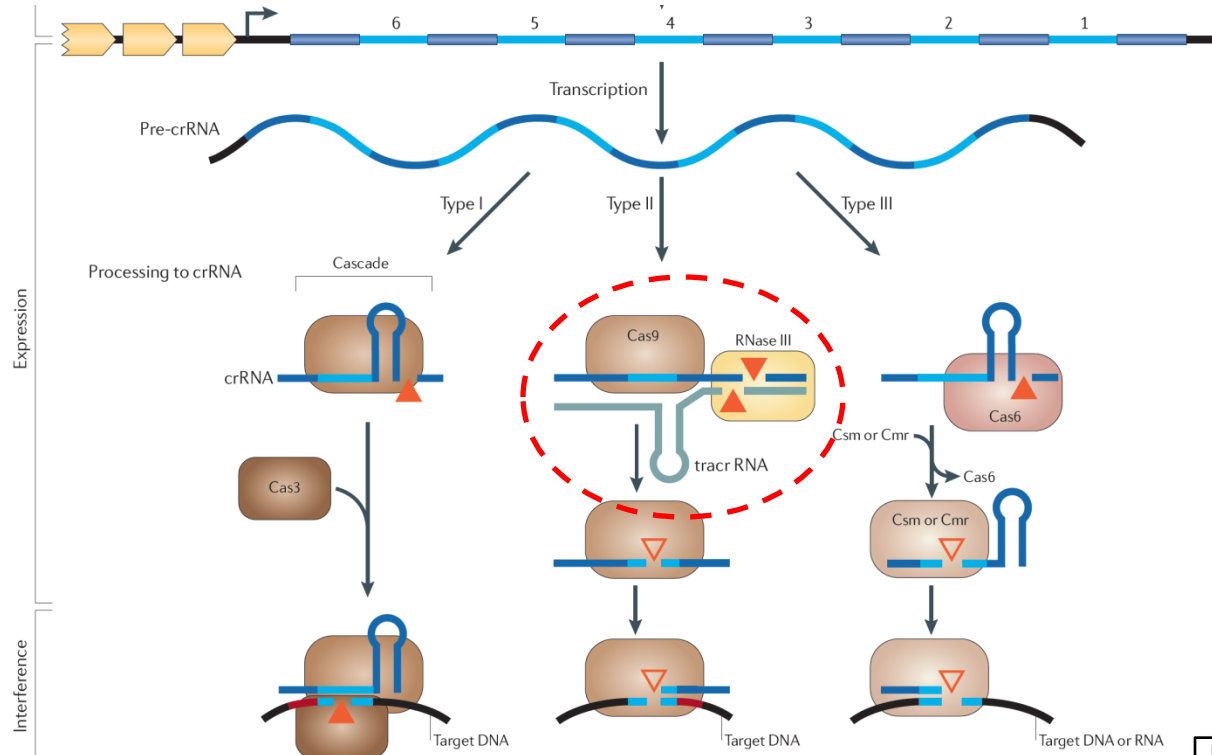
- clustered regularly interspaced short palindromic repeats
- found in 90 % of archaea and 40 % of bacteria
- direct repeats + spacers
- cas gene (CRISPR-associated)
- proto-spacer adjacent motif (PAM)



background - CRISPR

the adaptive immune system of bacteria and archaea

- pre-crRNA processed into crRNAs (23-47 nt)
- matches proto-spacer of invading nucleic acid
- Type II uses a trans-encoded small RNA (tracrRNA)

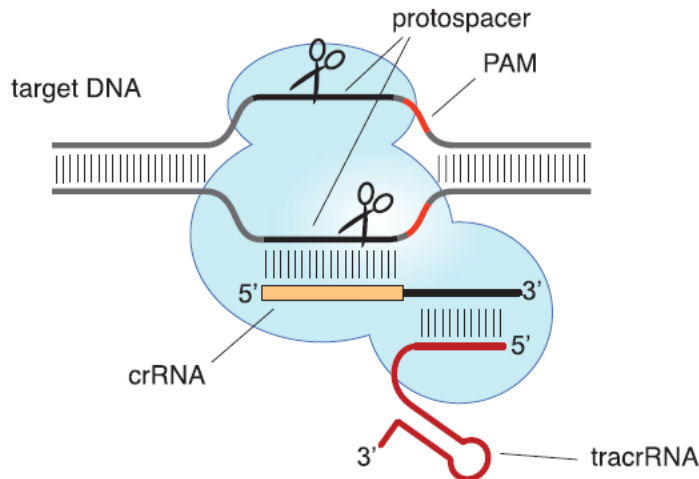


background - CRISPR

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Cas9 programmed by crRNA:tracrRNA duplex



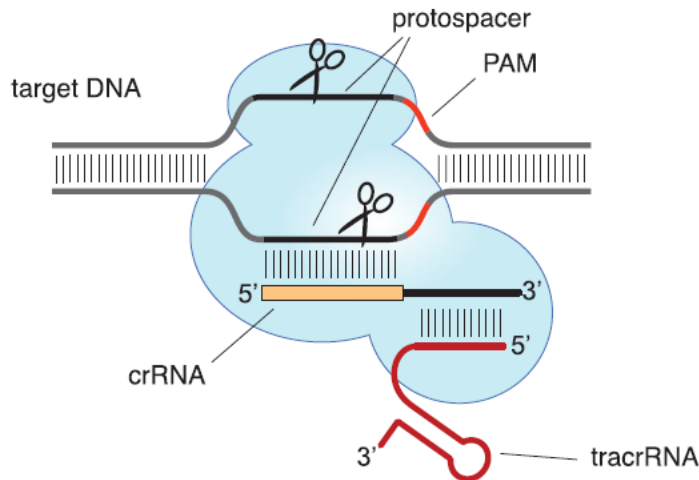
A Programmable Dual-RNA-Guided DNA Endonuclease in Adaptive Bacterial Immunity
Martin Jinek *et al.*
SCIENCE VOL 337 17 AUGUST 2012

background - CRISPR

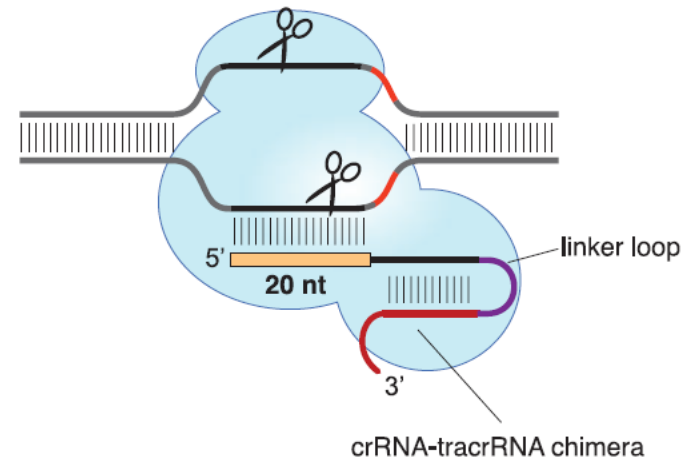
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Cas9 programmed by crRNA:tracrRNA duplex



Cas9 programmed by single chimeric RNA



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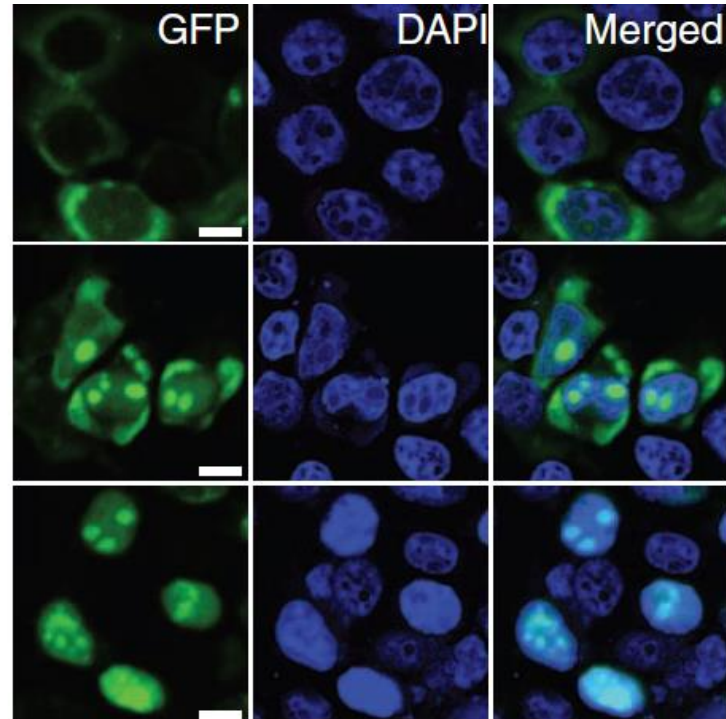
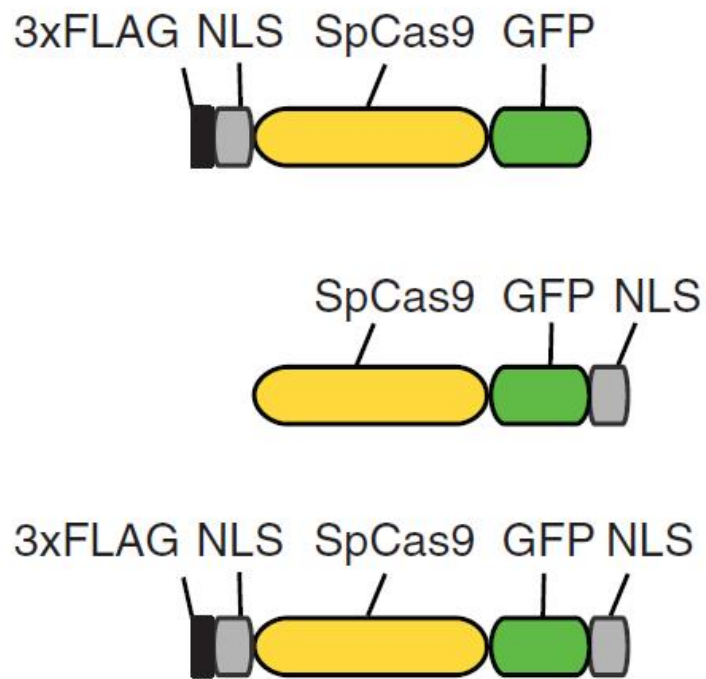
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construction of the system

type II CRISPR locus from *S. pvogenes*

- codon-optimized Cas9
- introduced NLS

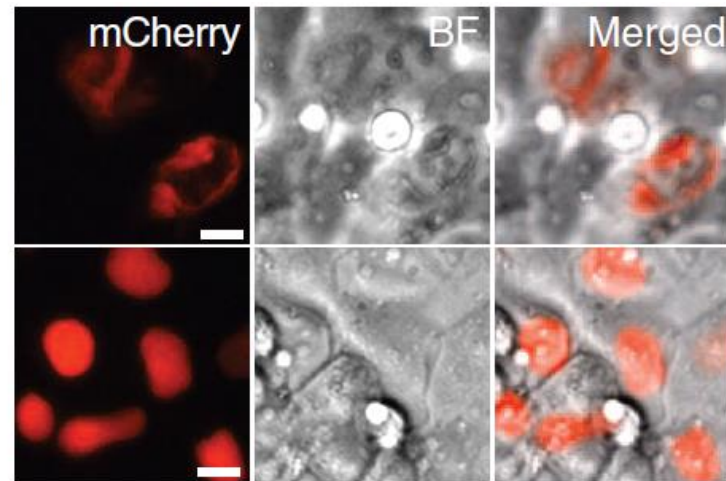
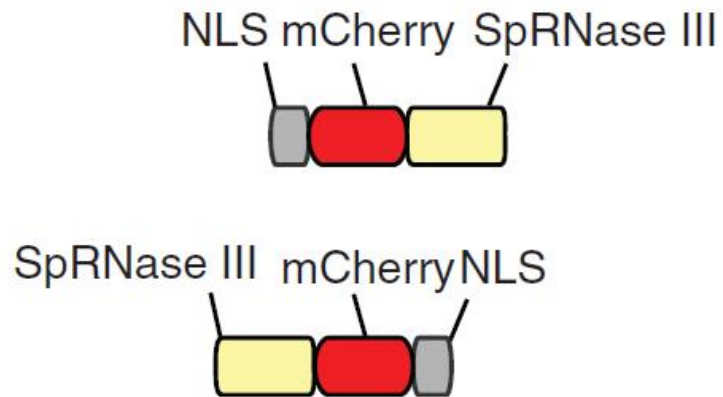


Le Cong *et al.*

construction of the system

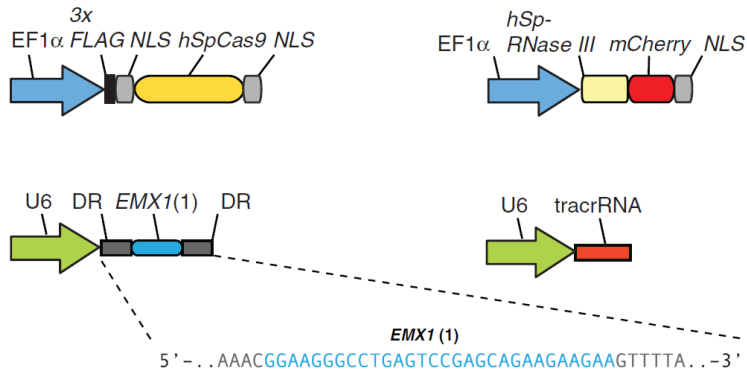
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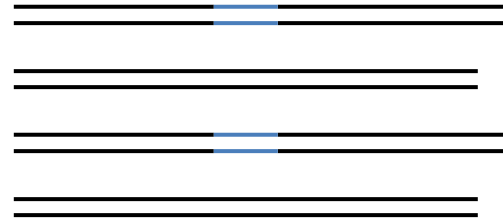
Le Cong *et al.*

first tests (NHEJ)

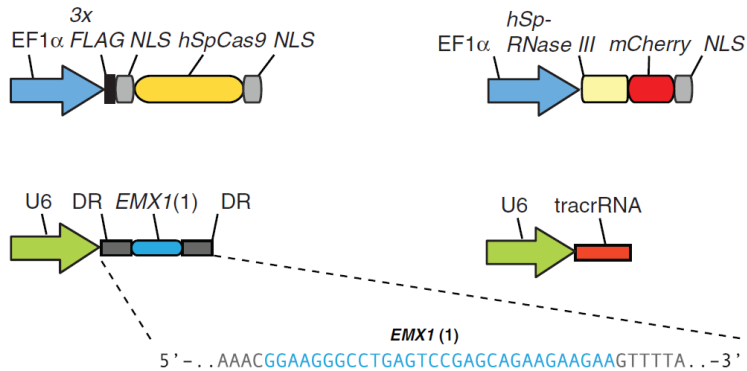


- transiently express constructs in HEK293
- pooled genomic DNA
- amplified EMX locus
- **survey assay**
 - denature DNA

denature

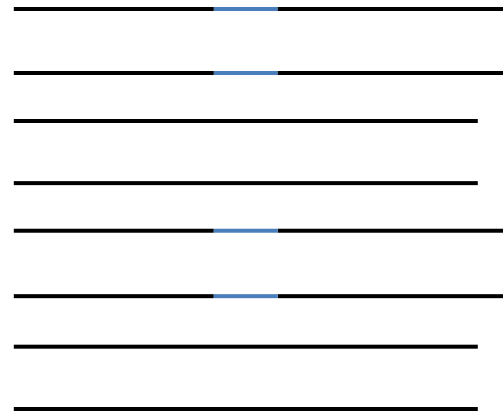


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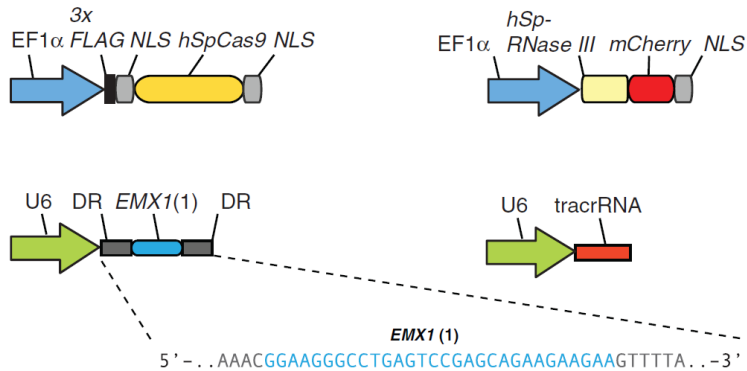


- transiently express constructs in HEK293
- pooled genomic DNA
- amplified EMX locus
- **survey assay**
 - denature and re-anneal DNA

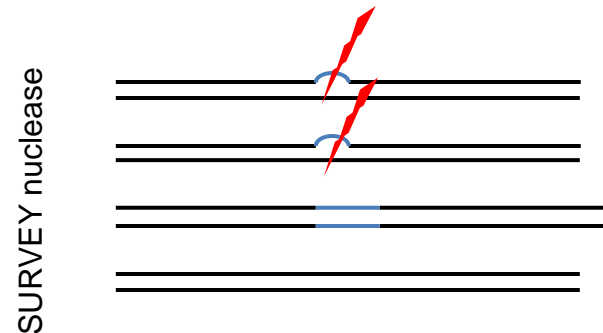
re-anneal



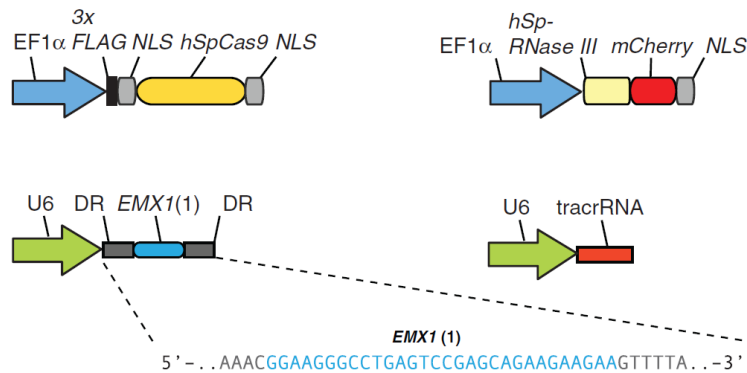
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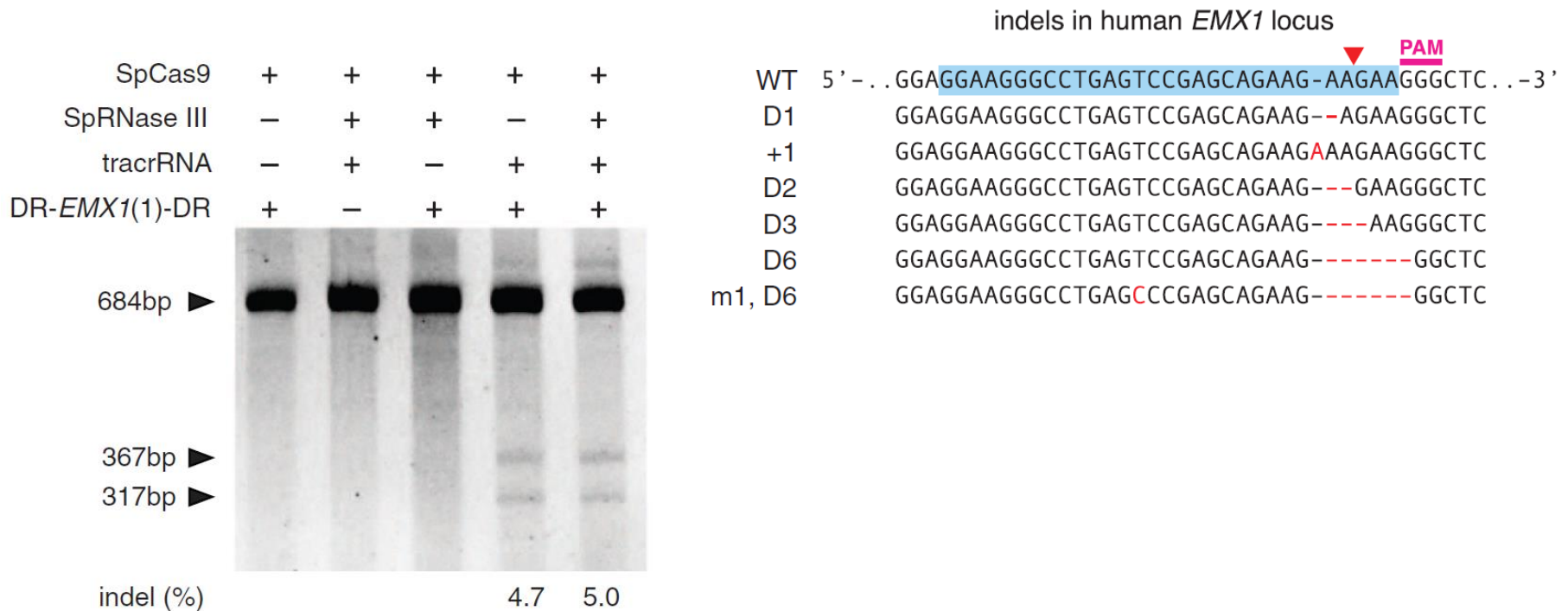
- transiently express constructs in HEK293
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- **survey assay**
 - denature and re-anneal DNA
 - heteroduplexes are cut by SURVEY nuclease



first tests (NHEJ)



- transiently express constructs in HEK293
- pooled genomic DNA
- amplified EMX locus
- survey assay**
 - denature and re-anneal DNA
 - heteroduplexes are cut by SURVEY nuclease
- Sanger seq



EF1 α 3x FLAG NLS hSpCas9 NLS

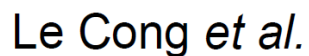
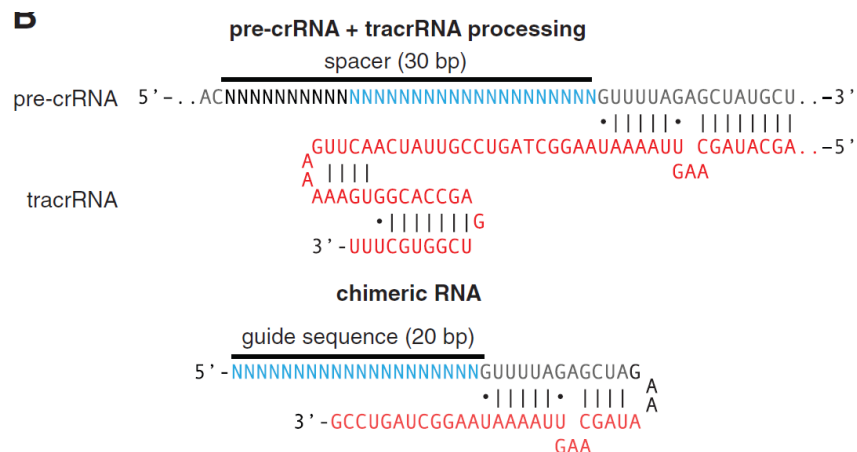
EF1 α RNase III mCherry NLS

U6 DR EMX1(1) DR

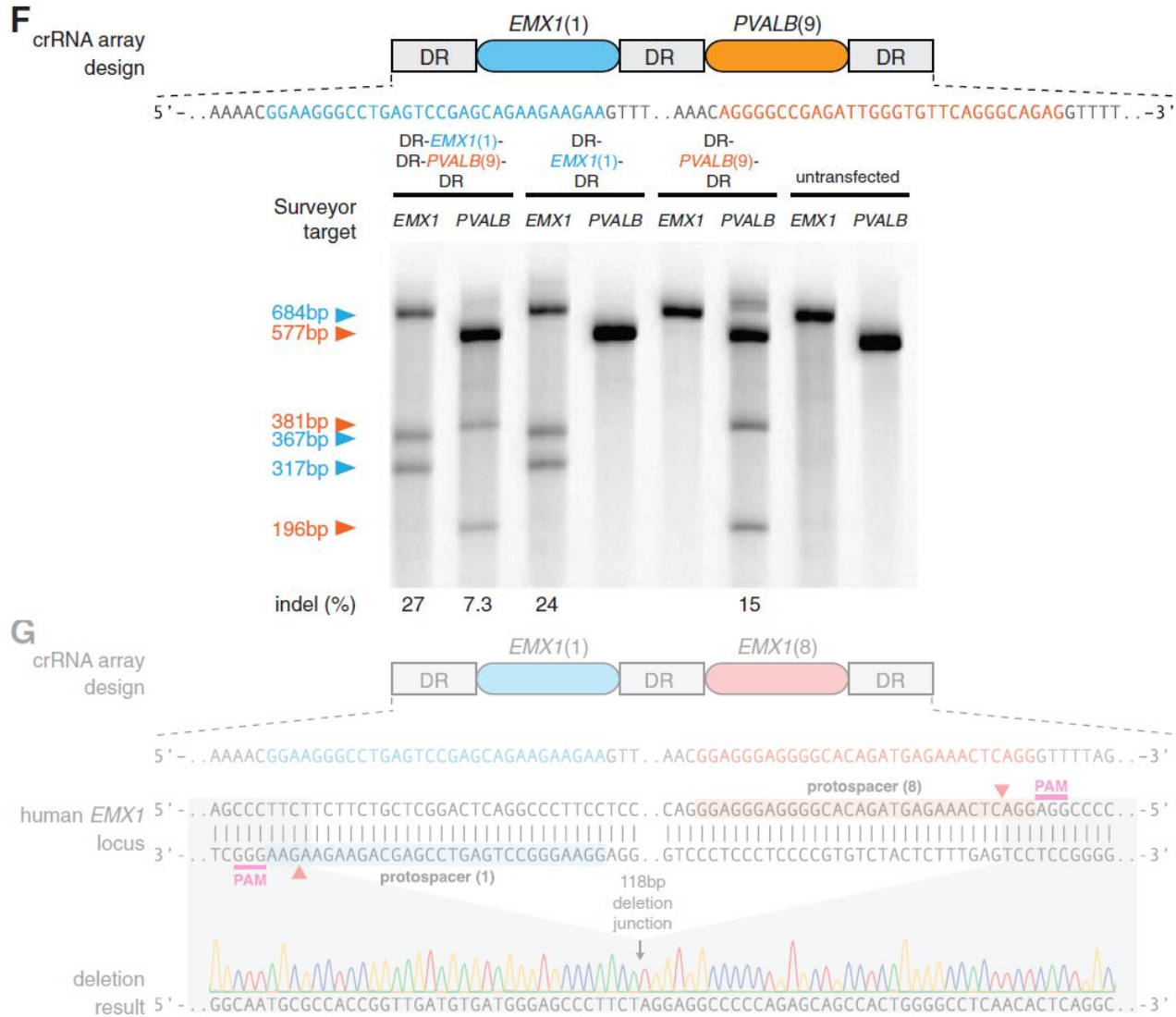
U6 tracrRNA

EMX1 (1)

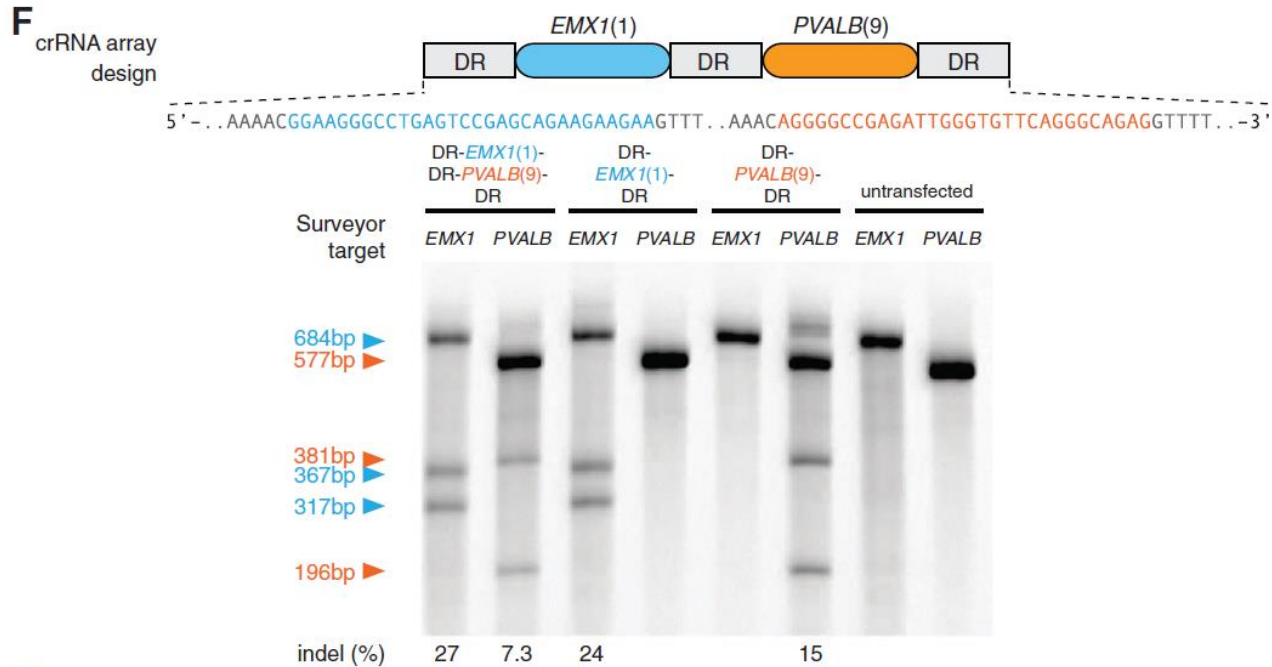
5' - ...AAACGGAAGGGCCTGAGTCCGAGCAGAAGAAGAGTTTAA... - 3'



array design (NHEJ)

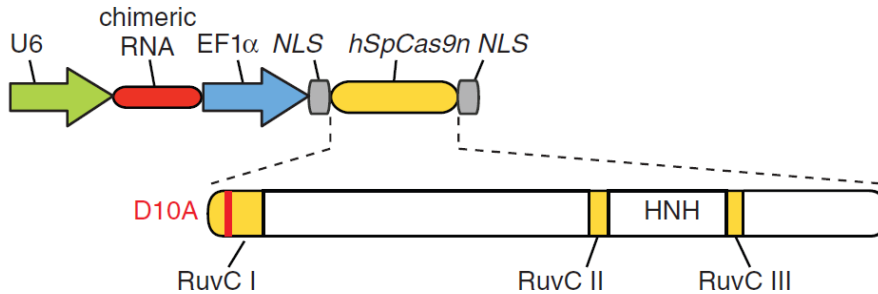


array design (NHEJ)



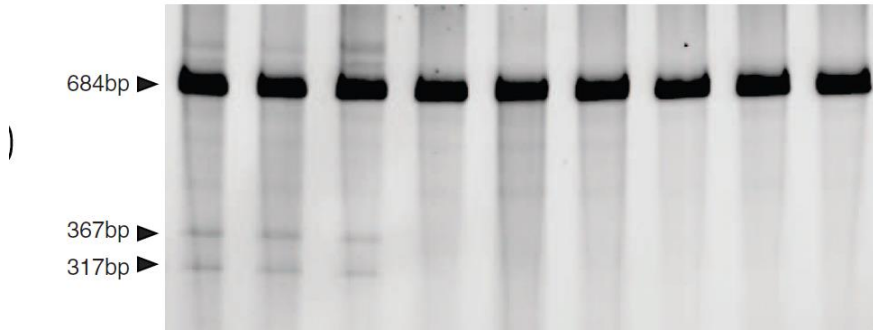
1.6 % deletion efficiency

homologous recombination



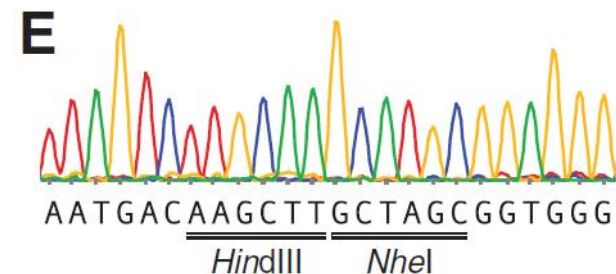
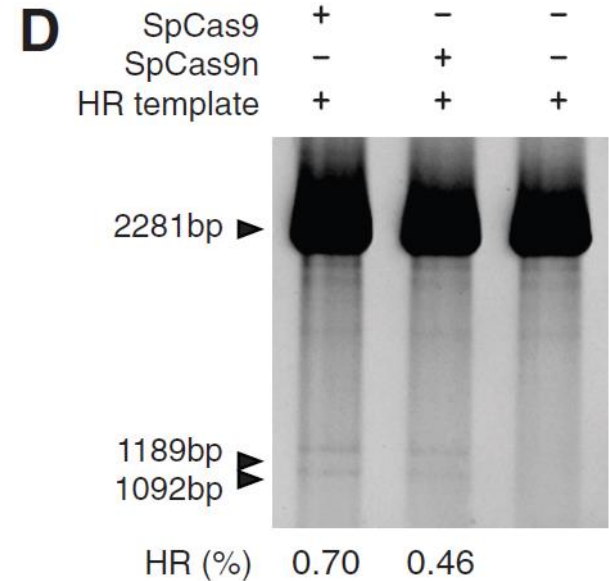
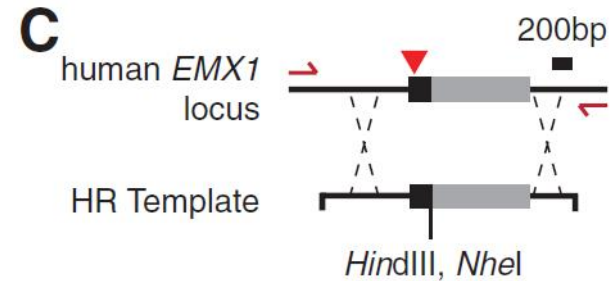
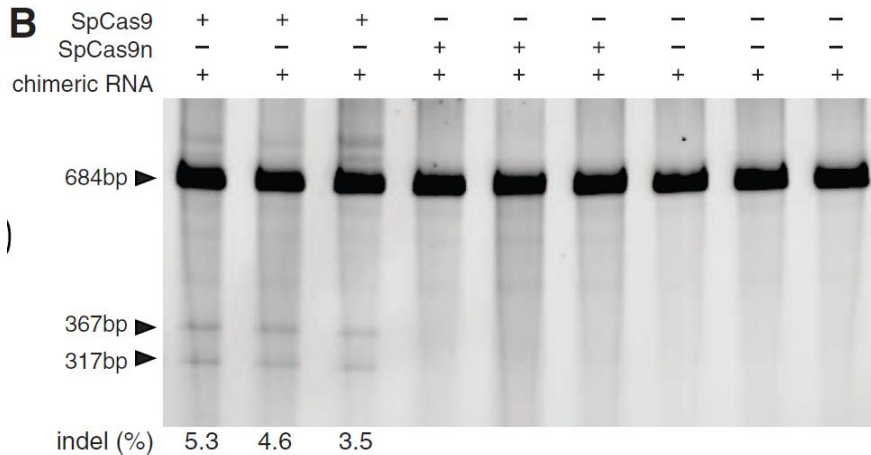
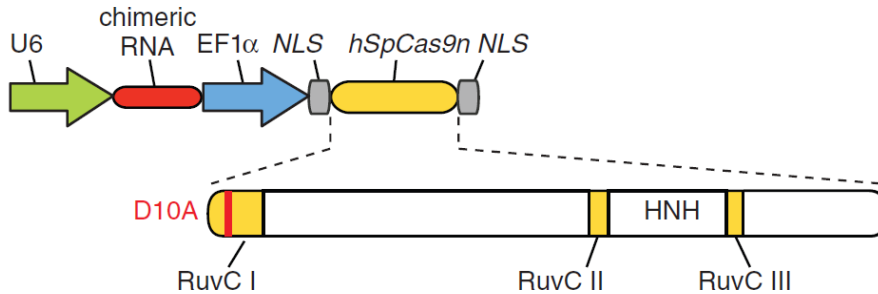
B

SpCas9	+	+	+	-	-	-	-	-	-
SpCas9n	-	-	-	+	+	+	-	-	-
chimeric RNA	+	+	+	+	+	+	+	+	+



indel (%) 5.3 4.6 3.5

homologous recombination



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testing the system (NHEJ)

type II CRISPR locus from *S. pvogenes*

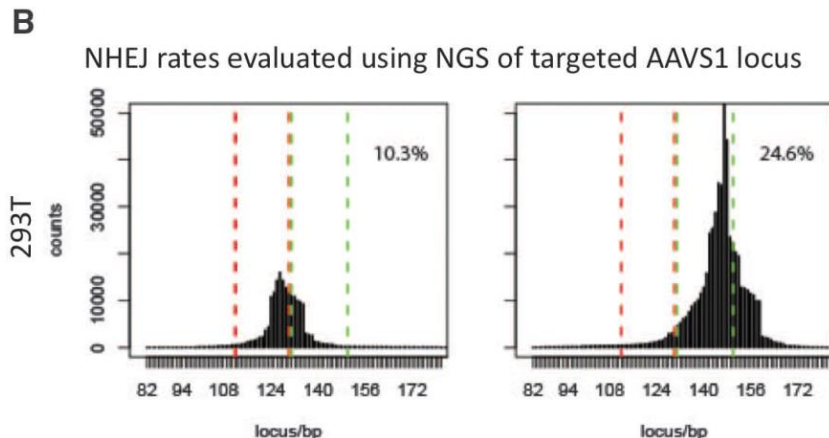
- codon-optimized Cas9
- introduced NLS
- transfected HEK293 cells
- MiSeq to analyze deletions
 - gDNA was pooled
 - target region was amplified
 - MiSeq

A

endogenous 'native' hAAVS1 locus sequence

. TTATCTGTCCTCCACCCACAGTGGGCCACTAGGGACAGGATTGGTGA. .

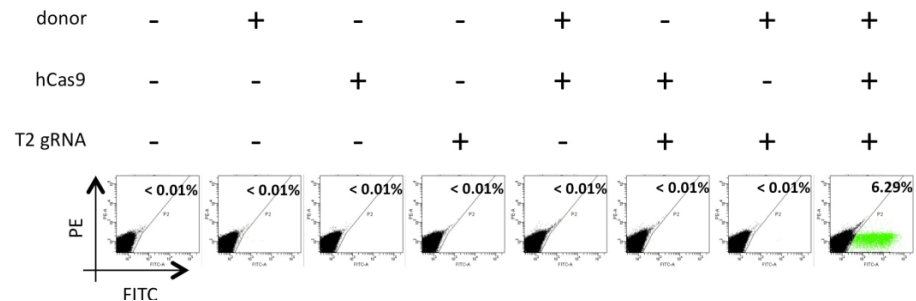
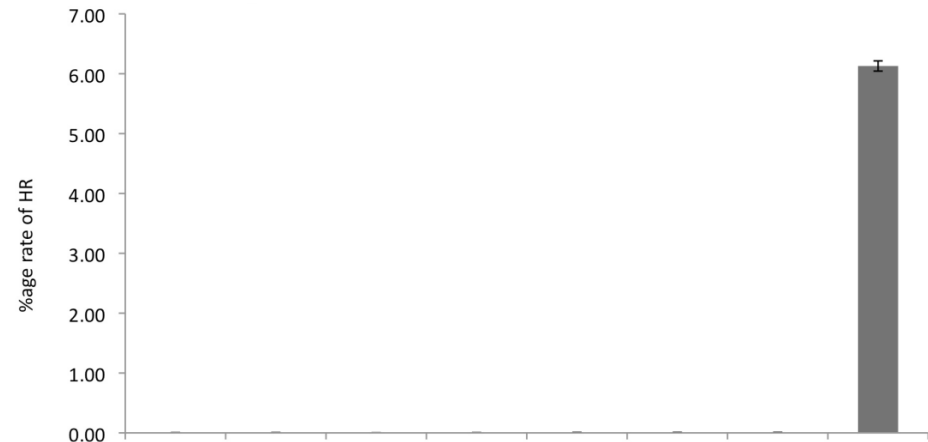
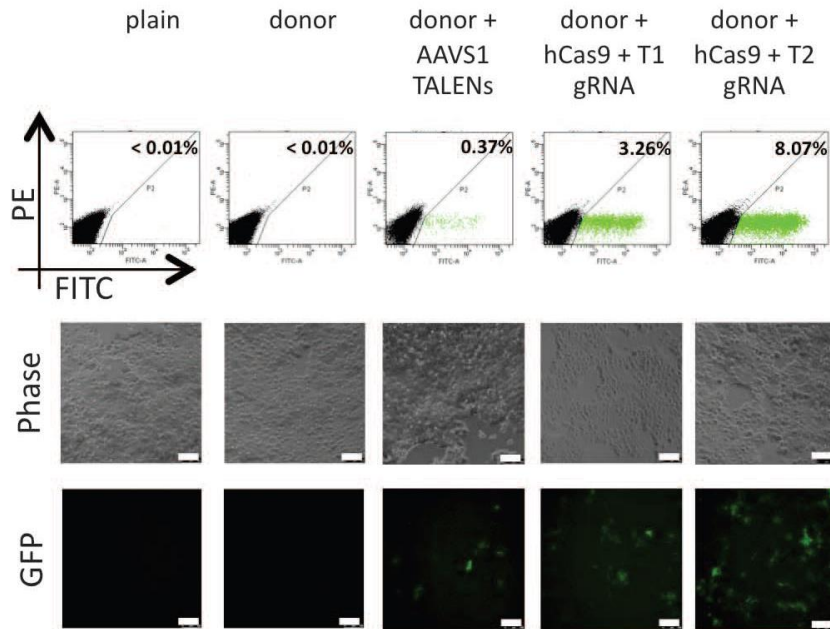
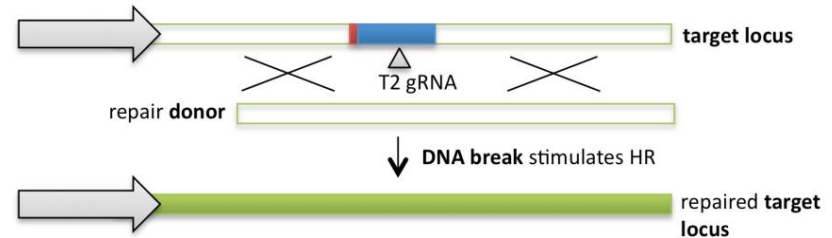
T1 target T2 target



homologous repair/specificity

GFP reporter assay in HEK293T

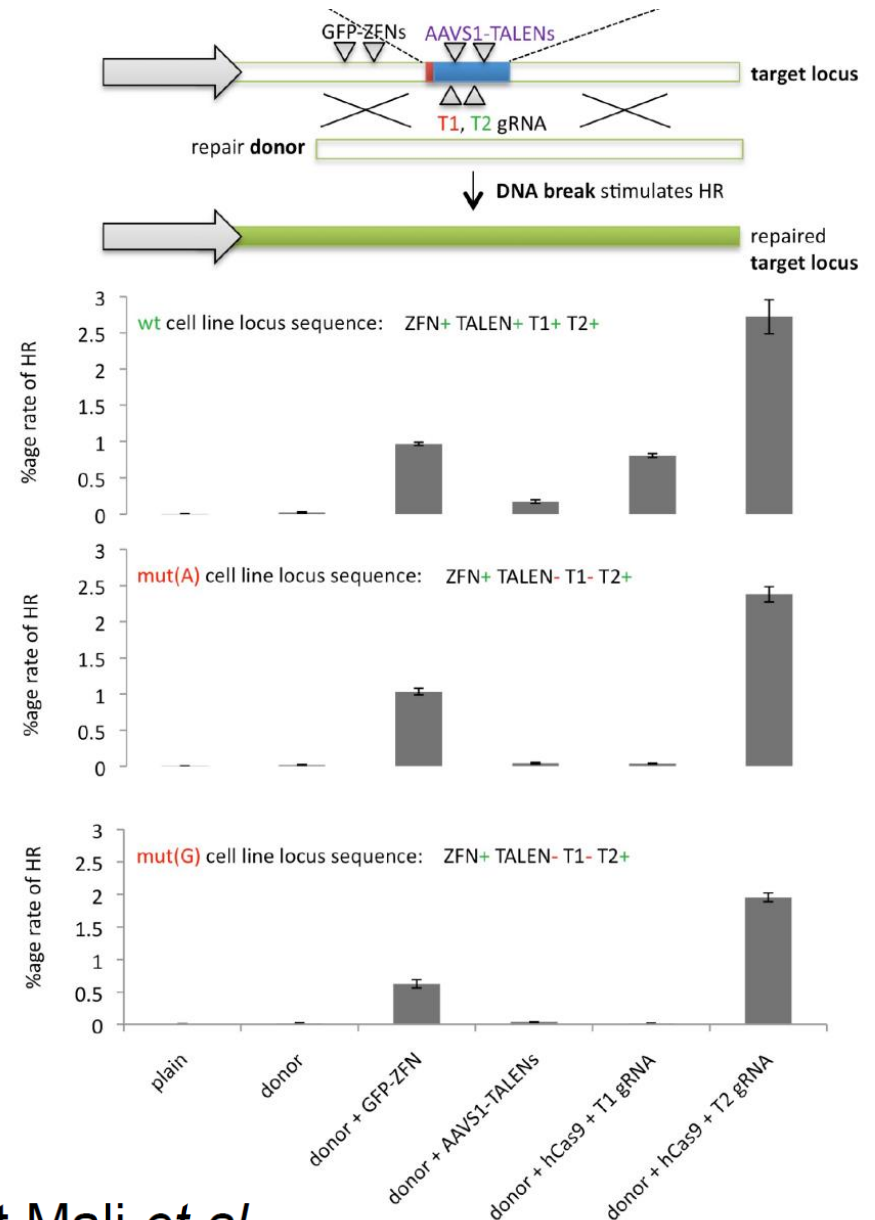
- stable cell line bearing disrupted GFP
 - insertion of stop
 - a 68 bp from AAVS1 locus
- repair donor to restore GFP expression



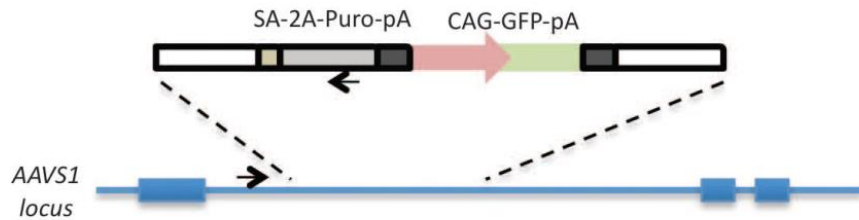
homologous repair/specificity

GFP reporter assay in HEK293T

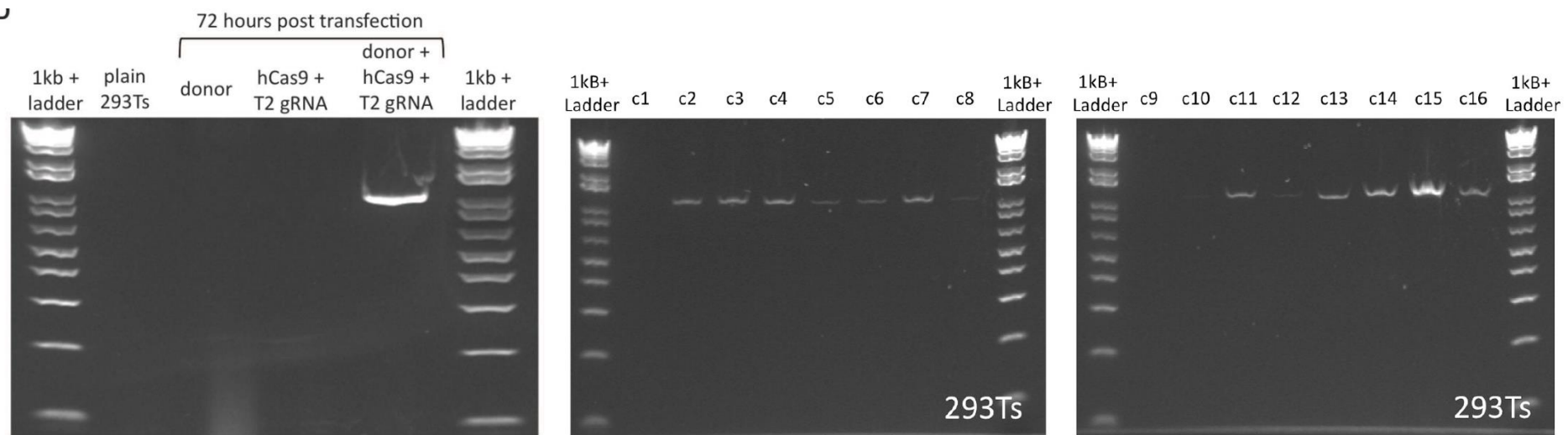
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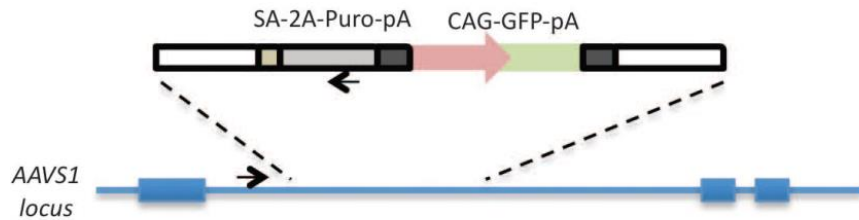
genome editing at endogenous locus



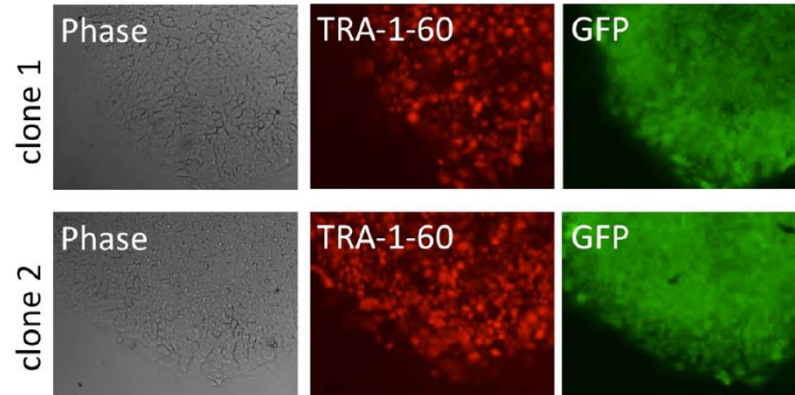
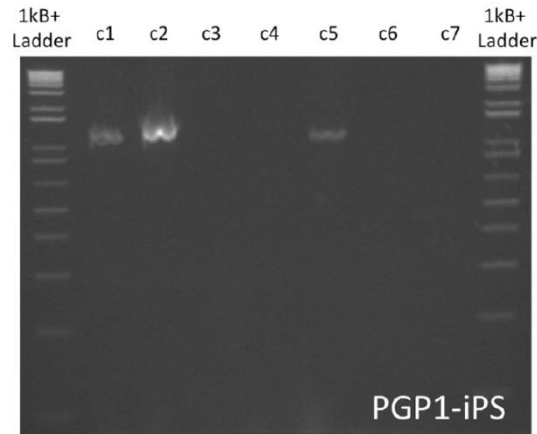
- target endogenous AAVS1 locus
- donor DNA
 - puromycin resistance
 - GFP
- selection of single clones for puromycin



genome editing at endogenous locus



- target endogenous AAVS1 locus
- donor DNA
 - puromycin resistance
 - GFP
- selection of single clones for puromycin



**Thank you very much
for your attention!!!**

D10A mutation

endogenous 'native' hAAVS1 locus sequence
(293T)

..TTATCTGTCCCCTCCACCCACAGTGGGGCCACTAGGGACAGGATTGGTGA..
T2 target

NHEJ rates evaluated using NGS of targeted AAVS1 locus

